



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 12:39 PM UTC

PDB ID : 6JG3 / pdb_00006jg3
EMDB ID : EMD-9823
Title : Cryo-EM structure of RyR2 (Ca²⁺ alone dataset)
Authors : Chi, X.M.; Gong, D.S.; Ren, K.; Zhou, G.W.; Huang, G.X.Y.; Lei, J.L.; Zhou, Q.; Yan, N.
Deposited on : 2019-02-13
Resolution : 6.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

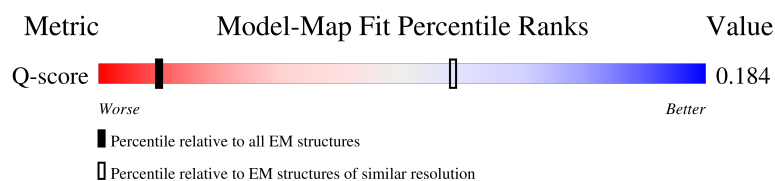
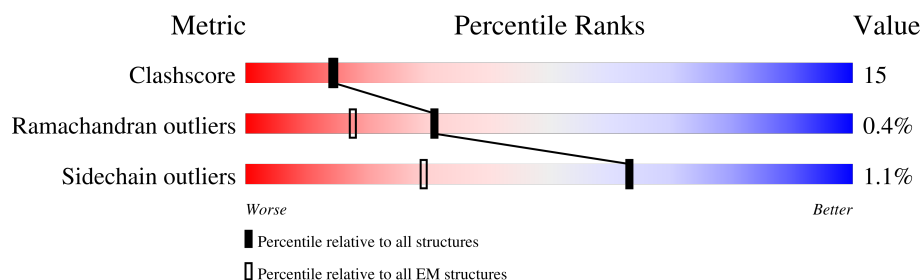
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	531 (5.60 - 6.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	4968	15% 47% 23% • 30%
1	B	4968	15% 47% 23% • 30%
1	C	4968	15% 47% 23% • 30%
1	D	4968	15% 46% 23% • 30%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 106185 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ryanodine receptor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3477	Total 26546	C 16893	N 4545	O 4951	S 157	0	0
1	B	3477	Total 26546	C 16893	N 4545	O 4951	S 157	0	0
1	C	3477	Total 26546	C 16893	N 4545	O 4951	S 157	0	0
1	D	3477	Total 26543	C 16890	N 4545	O 4951	S 157	0	0

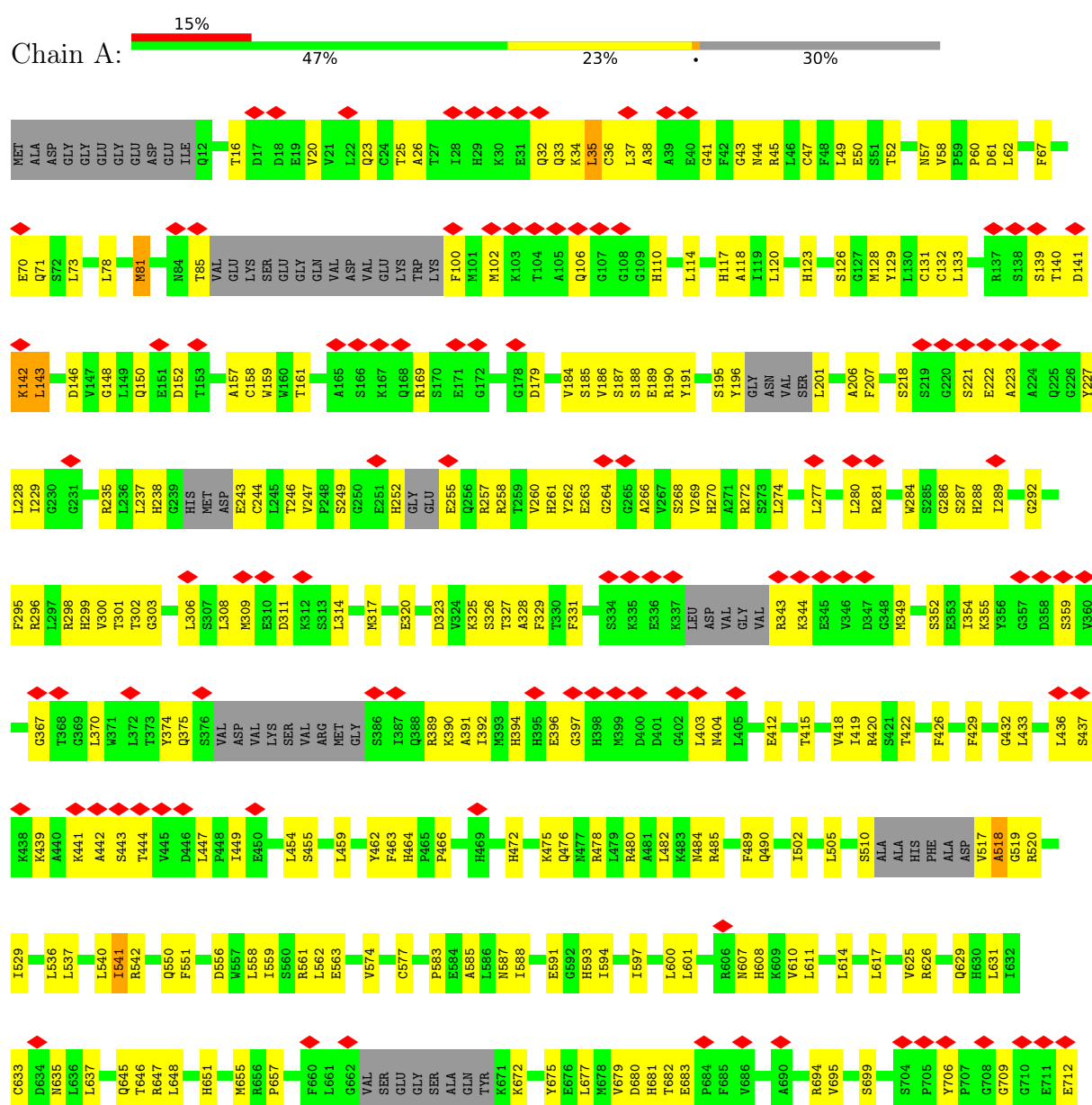
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

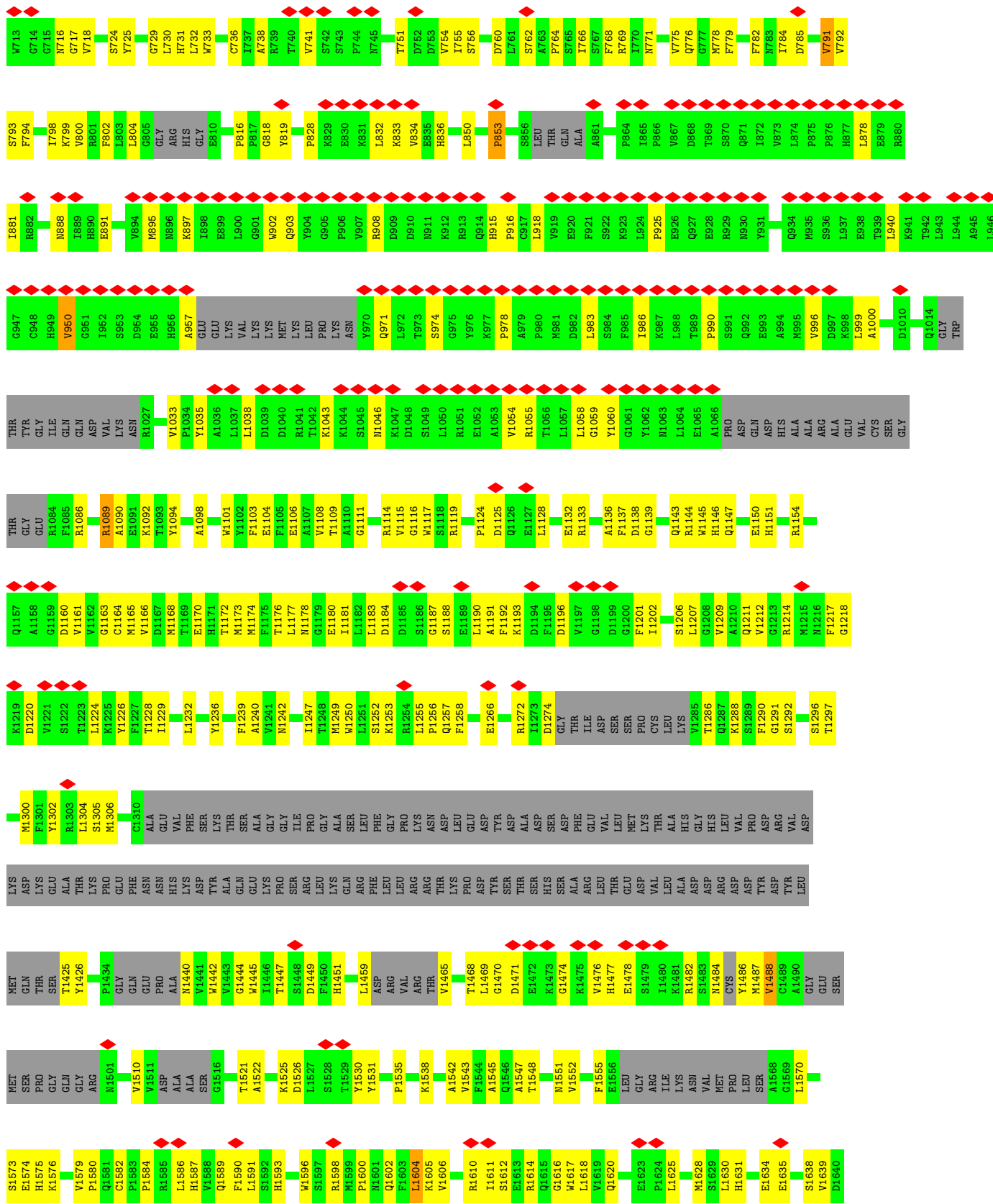
Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total 1	Zn 1	0
2	B	1	Total 1	Zn 1	0
2	C	1	Total 1	Zn 1	0
2	D	1	Total 1	Zn 1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ryanodine receptor 2



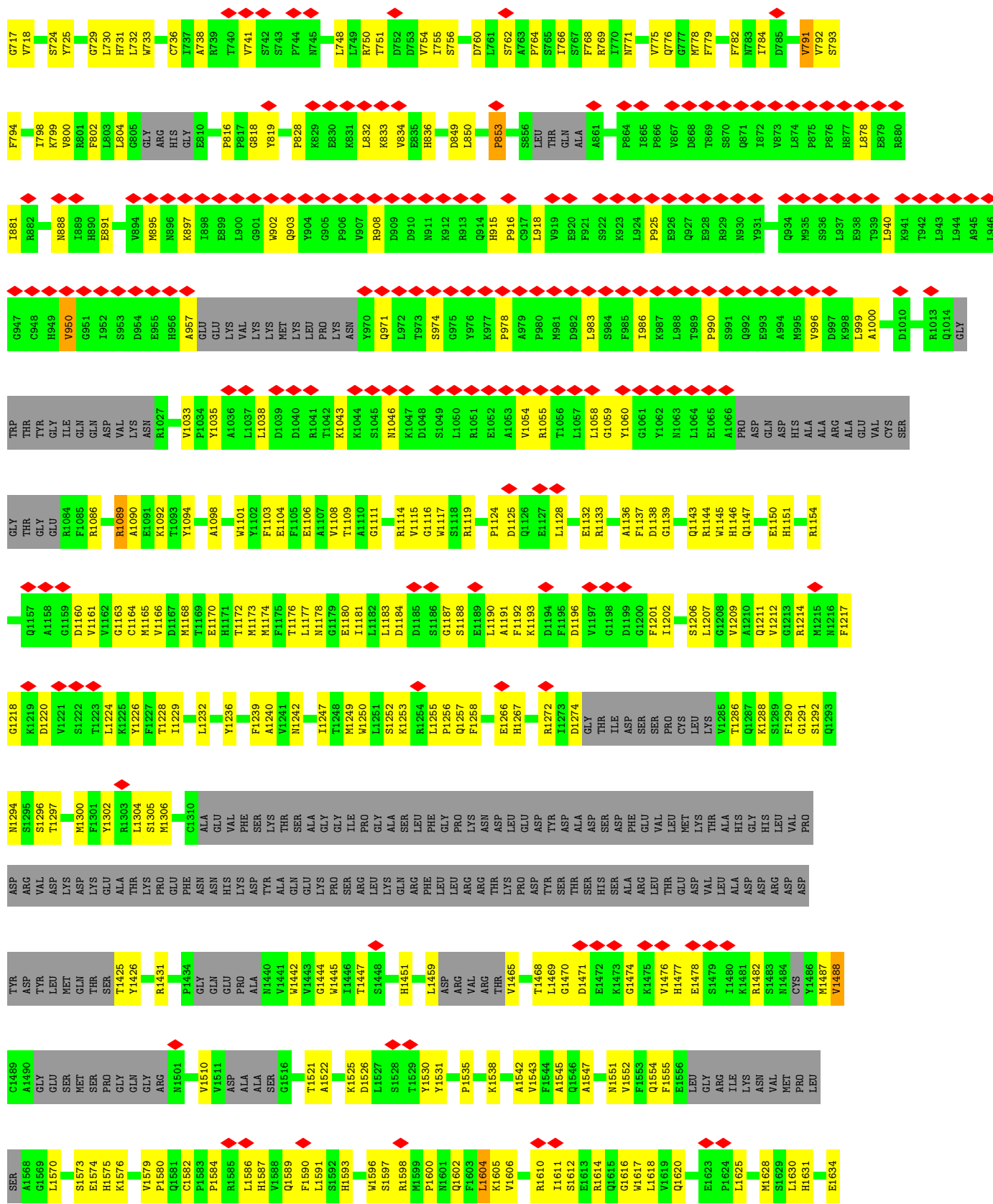








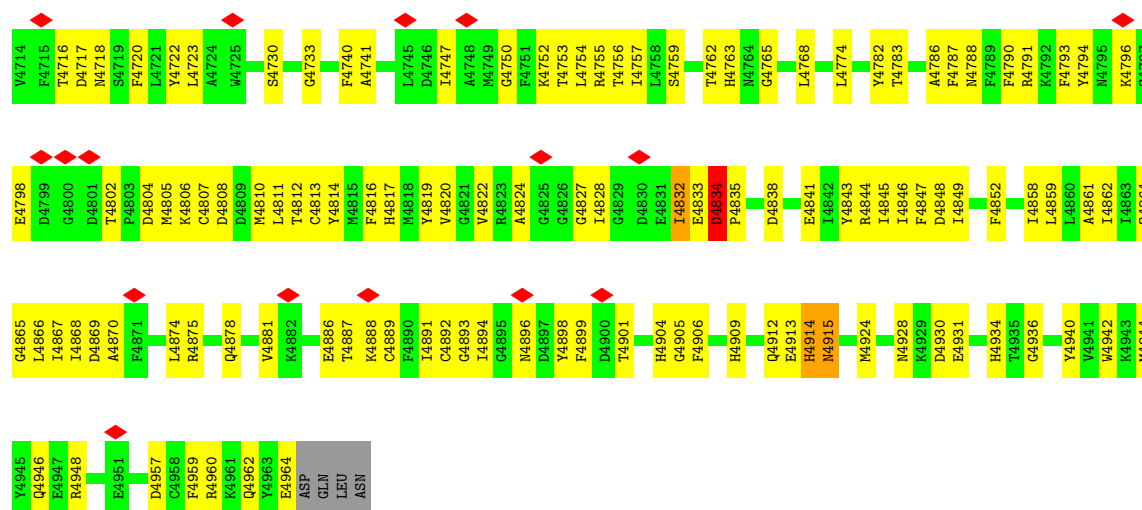




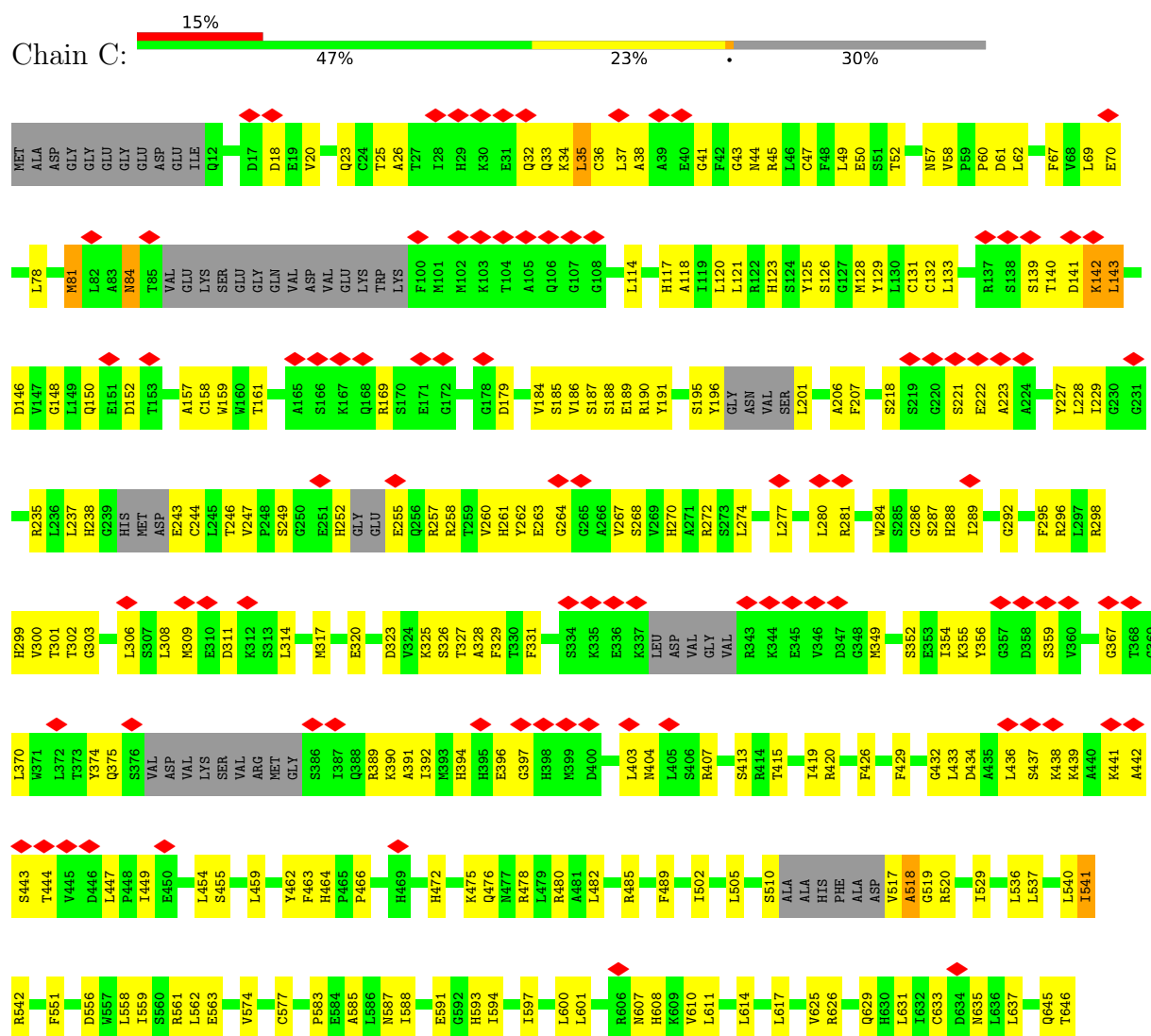








• Molecule 1: Ryanodine receptor 2

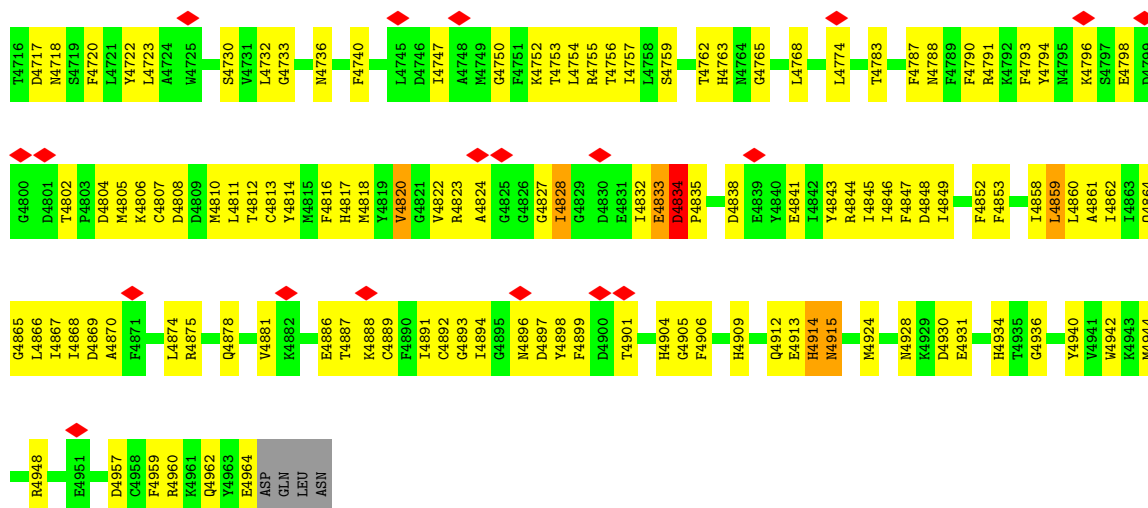




THR	ARG	CYS	ALA	PRO	L2535	F2536	A2537	G2538	L2549	V2553	TYR	ARG	LEU	SER	K2558	L2562	A2565	E2571	S2576	CYS	GLY	GLN	LEU	R2582	P2583	S2584	D2596	V2597	L2598	L2600	N2601	GLU	HIS	ALA	K2605	K2609	C2623	L2624	G2627	TRP	GLY	ASN	PHE	GLY	ALA	A2634	S2635									
THR	ILE	ALA	LYS	ASP	GLY	ASN	VAL	VAL	PRO	ASP	MET	SER	ALA	F2461	P2463	D2464	H2465	K2466	M2469	V2470	L2471	R2475	V2476	V2477	ILE	R2483	F2484	L2485	L2489	GLU	VAL	G2492	L2503	THR	ALA	ALA	LEU	SER	ALA	T2511	Y2520	L2521	C2522	T2523	L2529											
PRO	ASP	THR	GLU	GLY	GLU	ASP	ASP	THR	ILE	HIS	MET	G2386	N2387	A2388	F2392	R2402	G2403	A2404	PRO	GLU	MET	HIS	LEU	ILE	HIS	ALA	ALA	R2421	S2422	L2423	R2425	S2426	LEU	ILE	PRO	ASP	G2431	D2432	L2433	V2436	I2437	S2438	I2439	A2440	F2441	Q2442	MET	PRO								
G2296	E2297	R2298	Y2299	L2303	R2304	F2305	A2306	V2307	C2308	C2309	S2313	L2324	L2325	L2326	R2327	E2330	CYS	PHE	GLY	PRO	ALA	LEU	LEU	ARG	L2254	A2255	L2256	A2257	L2258	V2265	V2267	R2268	Y2269	L2270	L2275	GLN	SER	CYS	GLN	MET	LEU	VAL	SER	LYS	GLY	TYR	PRO	ASP	ILE	GLY	TRP	ASN	P2293			
A2214	M2215	H2218	Y2221	L2222	L2223	E2224	S2225	S2226	S2227	V2228	S2232	P2233	S2238	T2239	P2240	V2243	A2246	S2247	V2248	E2253	L2254	A2255	L2256	A2257	L2258	V2265	V2267	R2268	Y2269	L2270	L2275	GLN	SER	CYS	GLN	MET	LEU	VAL	SER	LYS	GLY	TYR	PRO	ASP	ILE	GLY	TRP	ASN	P2293							
I2118	L2121	A2122	S2123	Q2126	L2127	R2128	S2129	L2130	V2133	R2134	M2135	G2136	E2140	K2141	L2142	M2143	I2144	R2145	D2149	N2153	F2156	Y2157	Q2158	M2173	G2181	GLY	GLU	SER	LYS	ILE	THR	F2190	M2193	V2194	A2195	N2196	C2197	C2198	R2199	F2200	L2201	C2202	C2205	Q2212	K2213											
T2038	Y2039	L2040	LYS	LYS	GLN	ALA	GLU	LYS	VAL	GLU	SER	ASP	LYS	LYS	SER	T2058	L2059	L2062	L2063	T2066	M2067	V2070	V2075	M2085	F2086	L2088	L2089	R2090	R2091	D2094	G2095	L2096	V2100	R2101	A2102	L2103	F2104	K2105	T2106	Y2107	N2110	V2114	E2115	D2116	T2117											
PRO	GLN	GLU	GLN	ILE	ASN	MET	LEU	ASN	PHE	LYS	ASP	ASP	LYS	LYS	GLU	CYS	PRO	CYS	PRO	GLU	GLU	ILE	R1994	D1995	Q1996	L1997	D1998	D1999	D2003	E2011	L2012	D2013	GLU	ASP	GLY	SER	LEU	ASP	GLY	ASN	S2022	D2023	L2024	T2025	I2026	R2027	G2028	R2029	L2030	L2031	S2032	L2033	V2034	E2035	K2036	V2037
LEU	GLU	GLY	PRO	ALA	GLU	GLU	SER	LYS	GLY	LYS	ARG	PRO	LYS	LYS	GLU	CYS	K1898	L1899	P1900	K1904	Q1912	R1920	H1921	L1988	R1922	I1923	I1926	F1929	V1934	V1948	MET	GLN	ALA	LEU	ALA	LEU	THR	ALA	ARG	LYS	THR	LYS	GLU	PHE	ARG	SER	PRO									
R1807	D1808	G1811	F1816	V1819	P1820	K1823	Y1826	T1827	L1828	L1829	I1830	M1831	G1832	I1833	F1834	H1835	D1837	E1838	L1839	K1840	L1841	L1842	L1843	E1847	F1848	S1849	P1849	L1850	F1602	L1604	K1605	V1606	R1610	I1611	S1612	E1613	R1614	Q1615	G1616	M1617	Q1620	E1623	P1624	L1625	M1628	S1629	L1630	H1631	E1634	E1635						
SER	A1568	G1569	L1570	S1573	L1574	H1575	K1576	V1579	P1580	O1581	C1582	P1583	P1584	R1585	L1586	H1587	V1588	Q1589	F1590	L1591	S1592	H1593	W1596	S1597	R1598	W1599	P1600	N1601	Q1602	L1604	K1605	V1606	R1610	I1611	S1612	E1613	R1614	Q1615	G1616	M1617	Q1620	E1623	P1624	L1625	M1628	S1629	L1630	H1631	E1634	E1635						
LEU	GLU	GLY	PRO	ALA	GLU	GLU	SER	LYS	GLY	LYS	ARG	PRO	LYS	LYS	GLU	CYS	K1898	L1899	P1900	K1904	Q1912	R1920	H1921	L1988	R1922	I1923	I1926	F1929	V1934	V1948	MET	GLN	ALA	LEU	ALA	LEU	THR	ALA	ARG	LYS	THR	LYS	GLU	PHE	ARG	SER	PRO									
R1718	L1719	M1720	M1721	I1726	V1727	P1728	M1729	T1730	L1738	F1739	D1741	ASN	LYS	LYS	HIS	G1747	L1748	P1749	H1750	I1751	G1752	S1756	L1757	R1758	P1759	M1761	P1766	S1767	PHE	VAL	SER	ILE	ASN	M1773	Q1777	E1781	F1782	P1783	I1786	I1792	L1795	V1799	S1803	L1804												
S1638	V1639	I1641	L1642	E1643	L1644	T1645	E1646	Q1647	L1651	H1654	T1657	L1658	R1659	S1662	A1663	V1664	L1667	G1668	N1669	V1672	A1673	L1676	H1679	V1680	D1681	E1682	P1683	Q1684	L1685	L1686	Y1687	A1688	N1691	K1692	Y1693	M1694	G1696	R1699	Y1703	D1704	I1707	L1711														





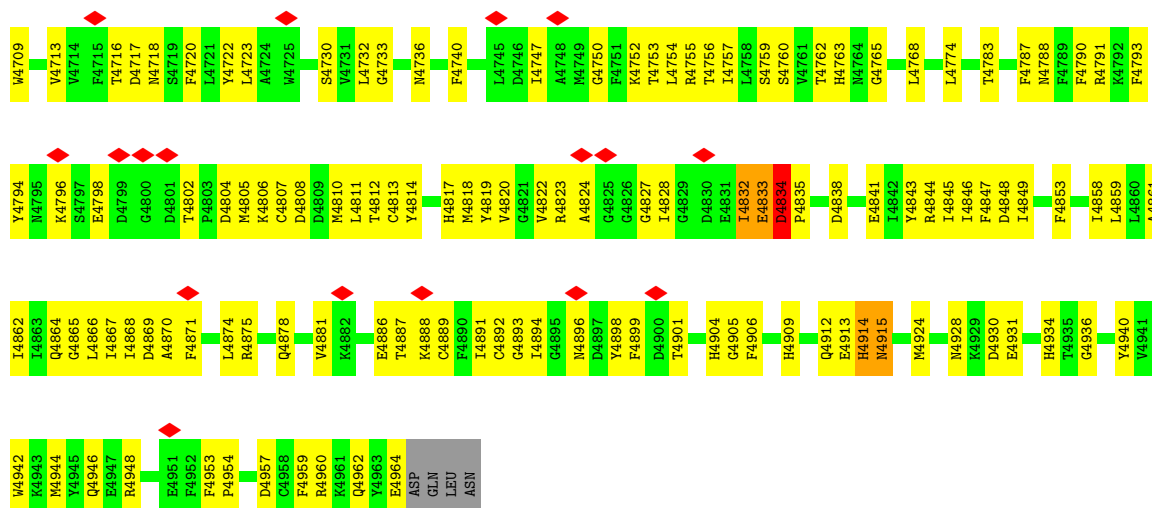












4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	24250	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48.6	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.258	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.065	Depositor
Map size (Å)	522.6, 522.6, 522.6	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.613, 2.613, 2.613	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.37	0/27034	0.71	26/36550 (0.1%)
1	B	0.37	0/27034	0.71	27/36550 (0.1%)
1	C	0.36	0/27034	0.72	30/36550 (0.1%)
1	D	0.37	0/27031	0.71	30/36546 (0.1%)
All	All	0.37	0/108133	0.71	113/146196 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	37
1	B	0	37
1	C	0	37
1	D	0	37
All	All	0	148

There are no bond length outliers.

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4833	GLU	CB-CA-C	9.63	125.81	109.53
1	C	4833	GLU	N-CA-C	-9.57	95.09	110.20
1	C	4820	VAL	CB-CA-C	-9.13	96.32	111.29
1	A	2156	PHE	N-CA-C	-9.10	101.08	113.18
1	B	2156	PHE	N-CA-C	-9.10	101.08	113.18

There are no chirality outliers.

5 of 148 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	141	ASP	Peptide
1	A	142	LYS	Peptide
1	A	221	SER	Peptide
1	A	518	ALA	Peptide
1	A	729	GLY	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	26546	0	25085	814	0
1	B	26546	0	25085	849	0
1	C	26546	0	25085	848	0
1	D	26543	0	25076	839	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	106185	0	100331	3153	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 3153 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:4820:VAL:O	1:D:4824:ALA:HB2	1.31	1.25
1:A:4783:THR:HG23	1:A:4817:HIS:CD2	1.75	1.21
1:B:4811:LEU:HB2	1:C:4519:LEU:CD1	1.71	1.18
1:A:4519:LEU:HD12	1:C:4811:LEU:HB2	1.28	1.16
1:B:4519:LEU:HD11	1:D:4811:LEU:HD13	1.28	1.13

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	3355/4968 (68%)	2934 (88%)	408 (12%)	13 (0%)	30	67
1	B	3355/4968 (68%)	2936 (88%)	407 (12%)	12 (0%)	30	67
1	C	3355/4968 (68%)	2934 (88%)	408 (12%)	13 (0%)	30	67
1	D	3355/4968 (68%)	2938 (88%)	405 (12%)	12 (0%)	30	67
All	All	13420/19872 (68%)	11742 (88%)	1628 (12%)	50 (0%)	31	67

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	LEU
1	B	143	LEU
1	C	143	LEU
1	D	143	LEU
1	A	142	LYS

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2678/4355 (62%)	2648 (99%)	30 (1%)	65	76
1	B	2678/4355 (62%)	2649 (99%)	29 (1%)	65	76
1	C	2677/4355 (62%)	2647 (99%)	30 (1%)	65	76
1	D	2676/4355 (61%)	2648 (99%)	28 (1%)	68	78
All	All	10709/17420 (62%)	10592 (99%)	117 (1%)	63	76

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4859	LEU
1	D	4632	ASP
1	C	1639	VAL
1	D	4561	VAL
1	D	1054	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 212 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	587	ASN
1	C	3919	ASN
1	D	3932	ASN
1	C	630	HIS
1	C	1684	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

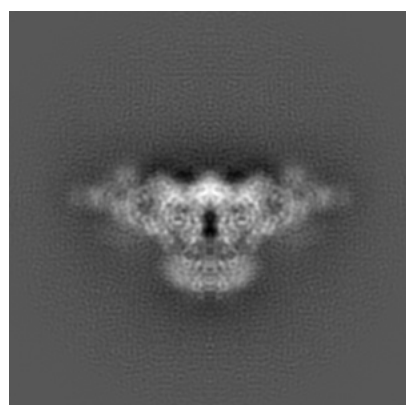
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9823. These allow visual inspection of the internal detail of the map and identification of artifacts.

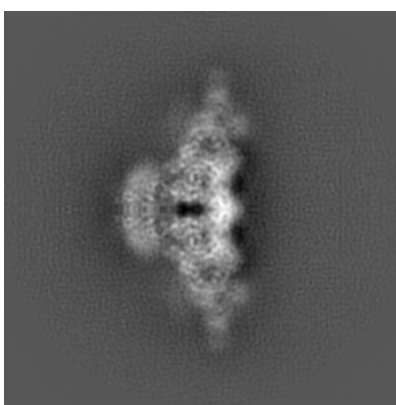
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

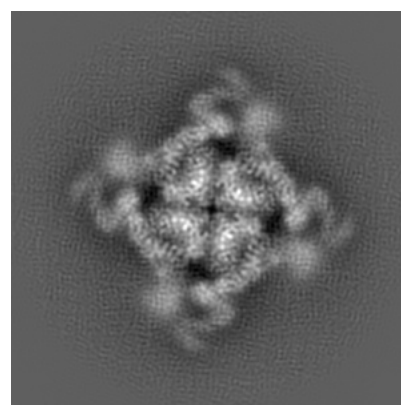
6.1.1 Primary map



X



Y

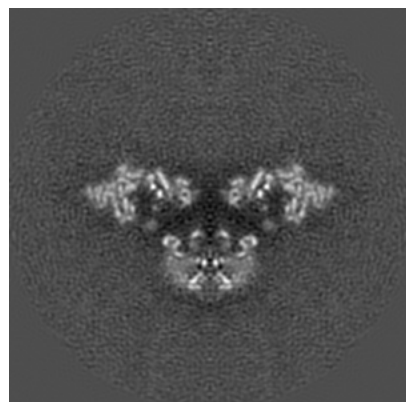


Z

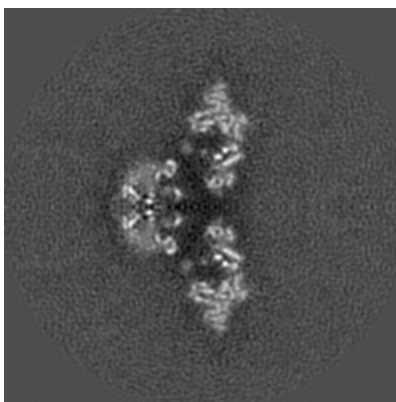
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

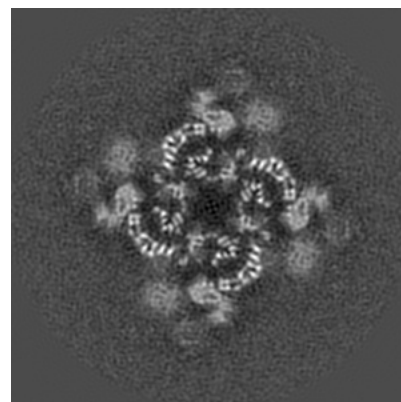
6.2.1 Primary map



X Index: 100



Y Index: 100

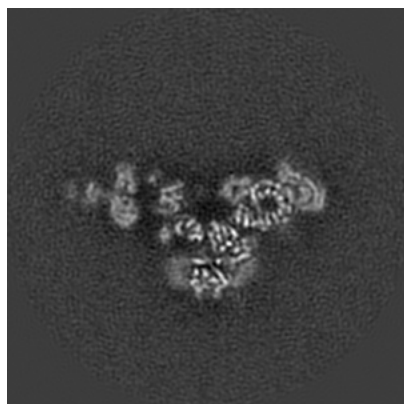


Z Index: 100

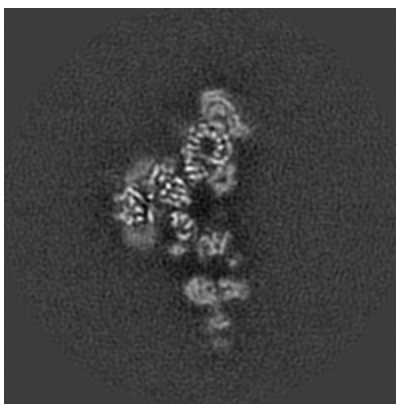
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

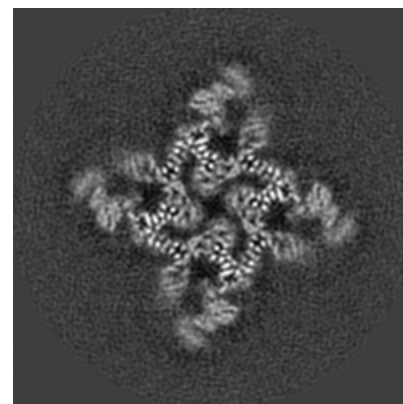
6.3.1 Primary map



X Index: 95



Y Index: 105

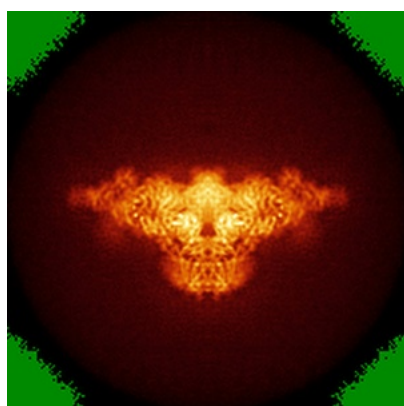


Z Index: 107

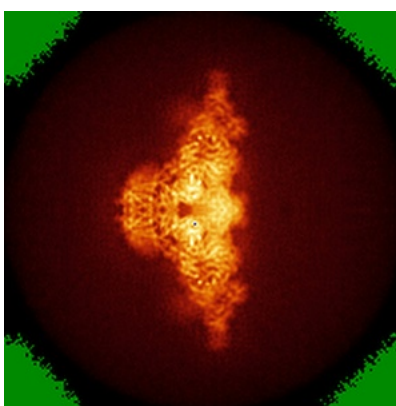
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

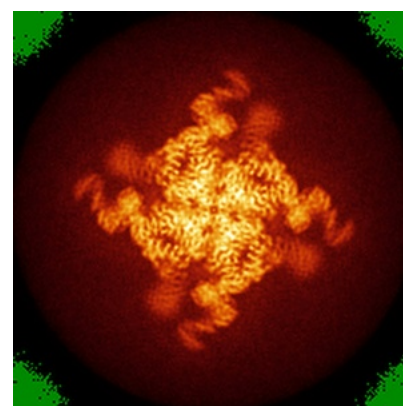
6.4.1 Primary map



X



Y

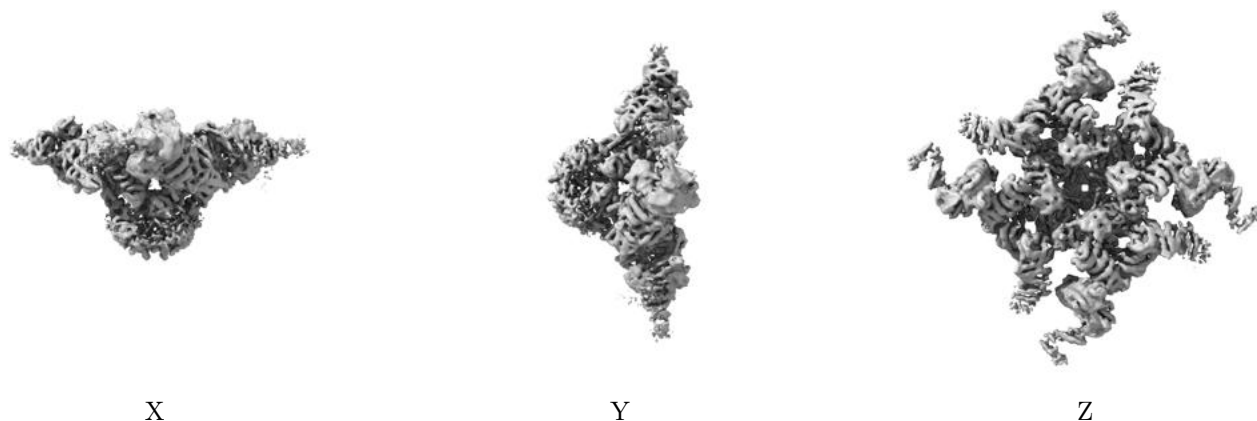


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

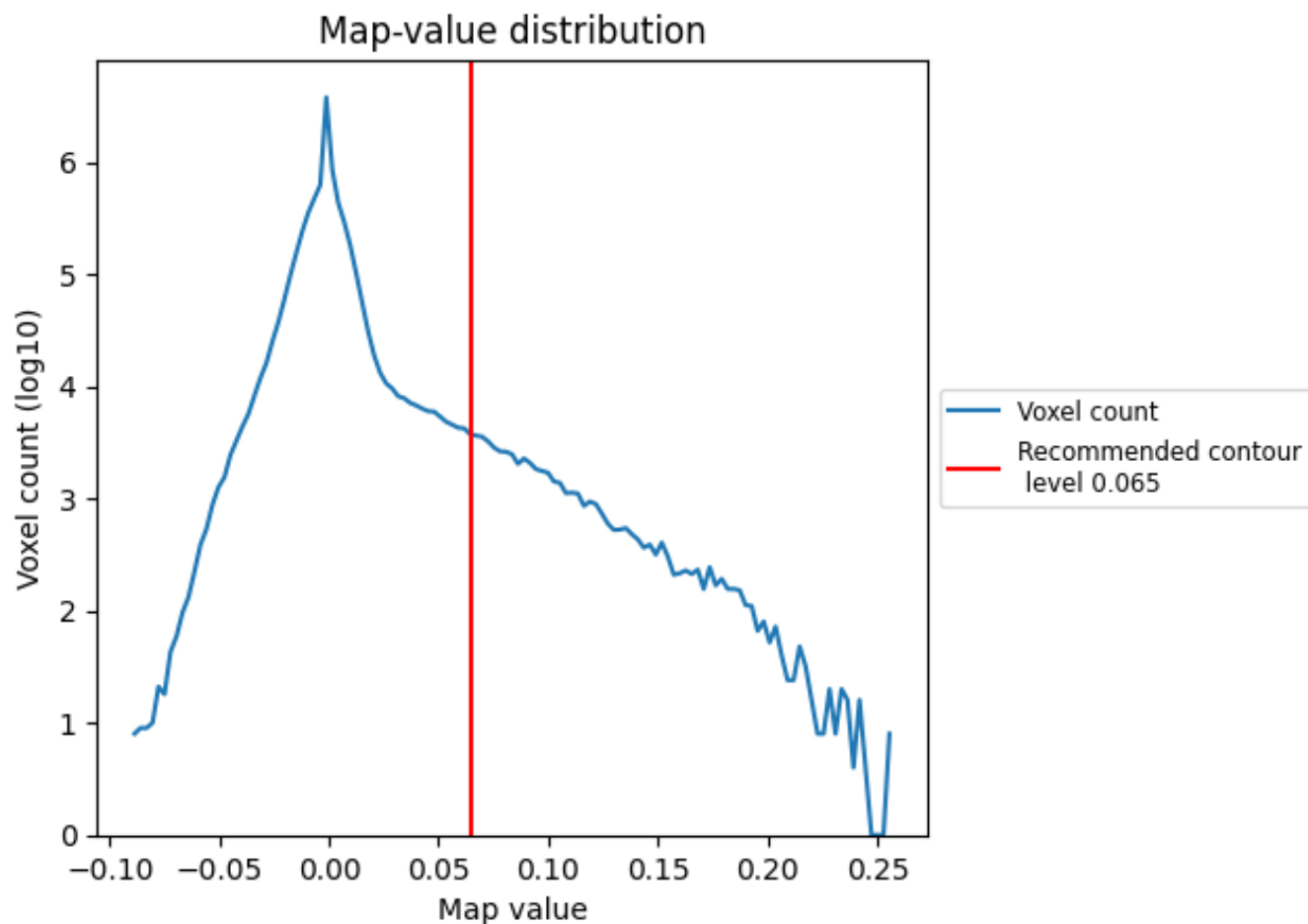
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

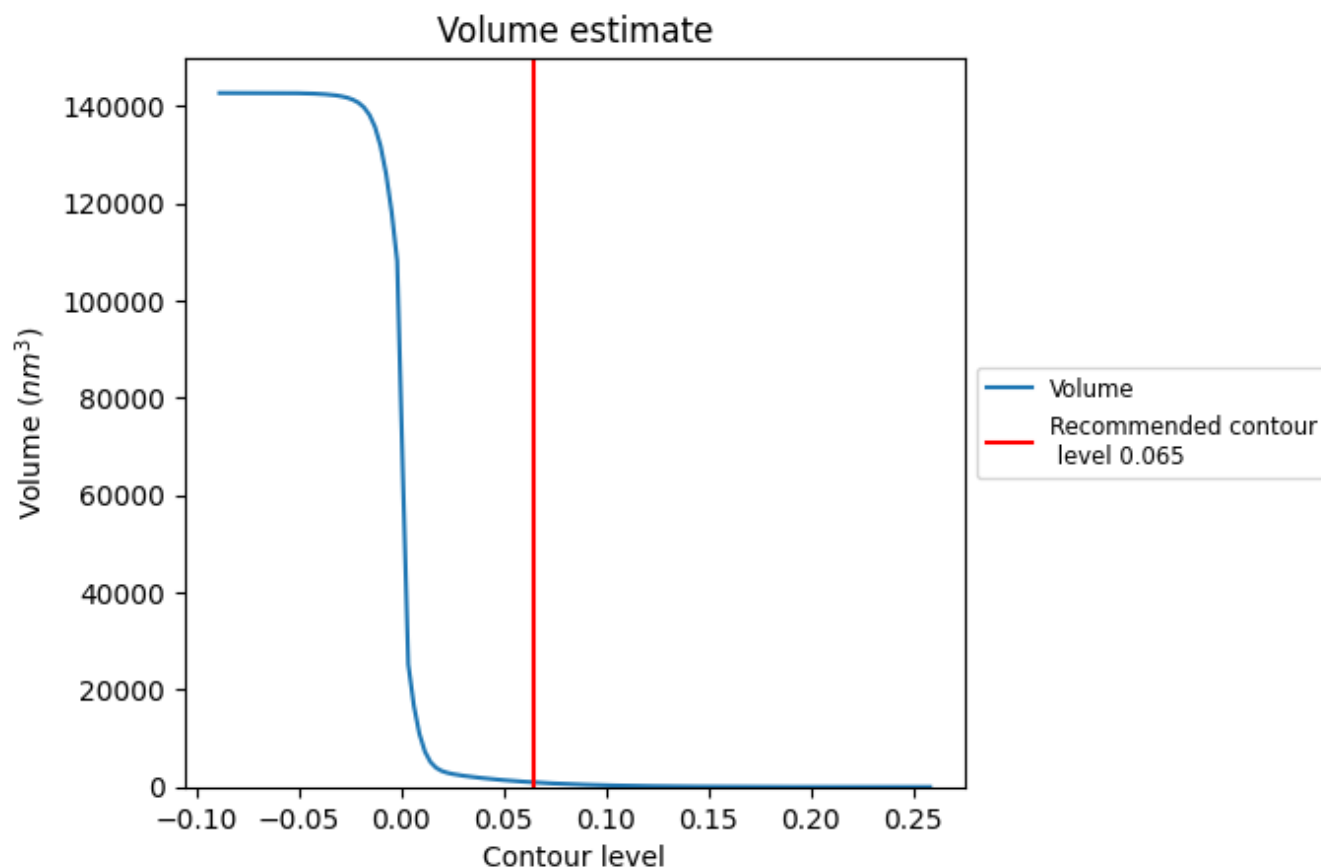
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

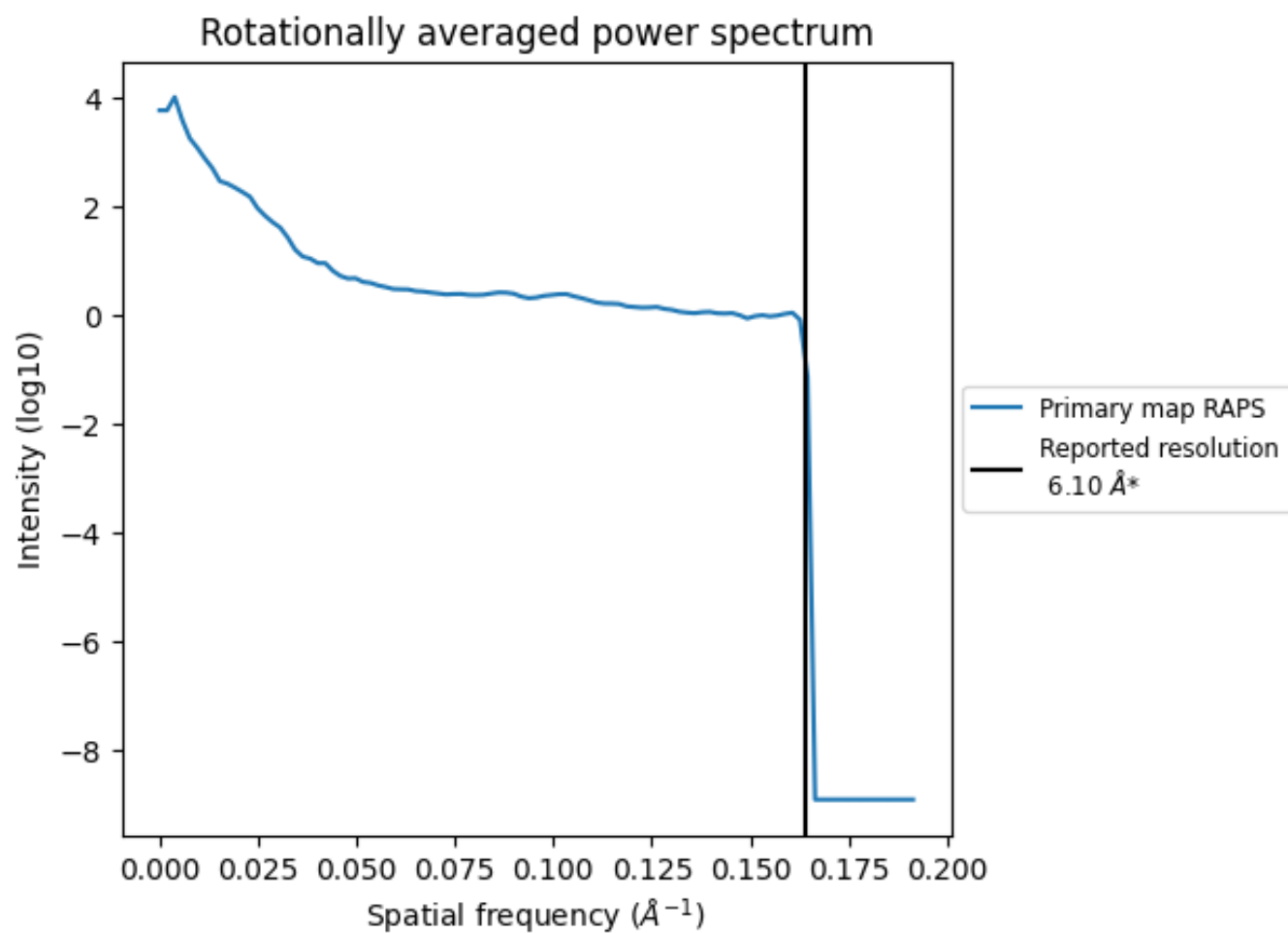
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 947 nm^3 ; this corresponds to an approximate mass of 855 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

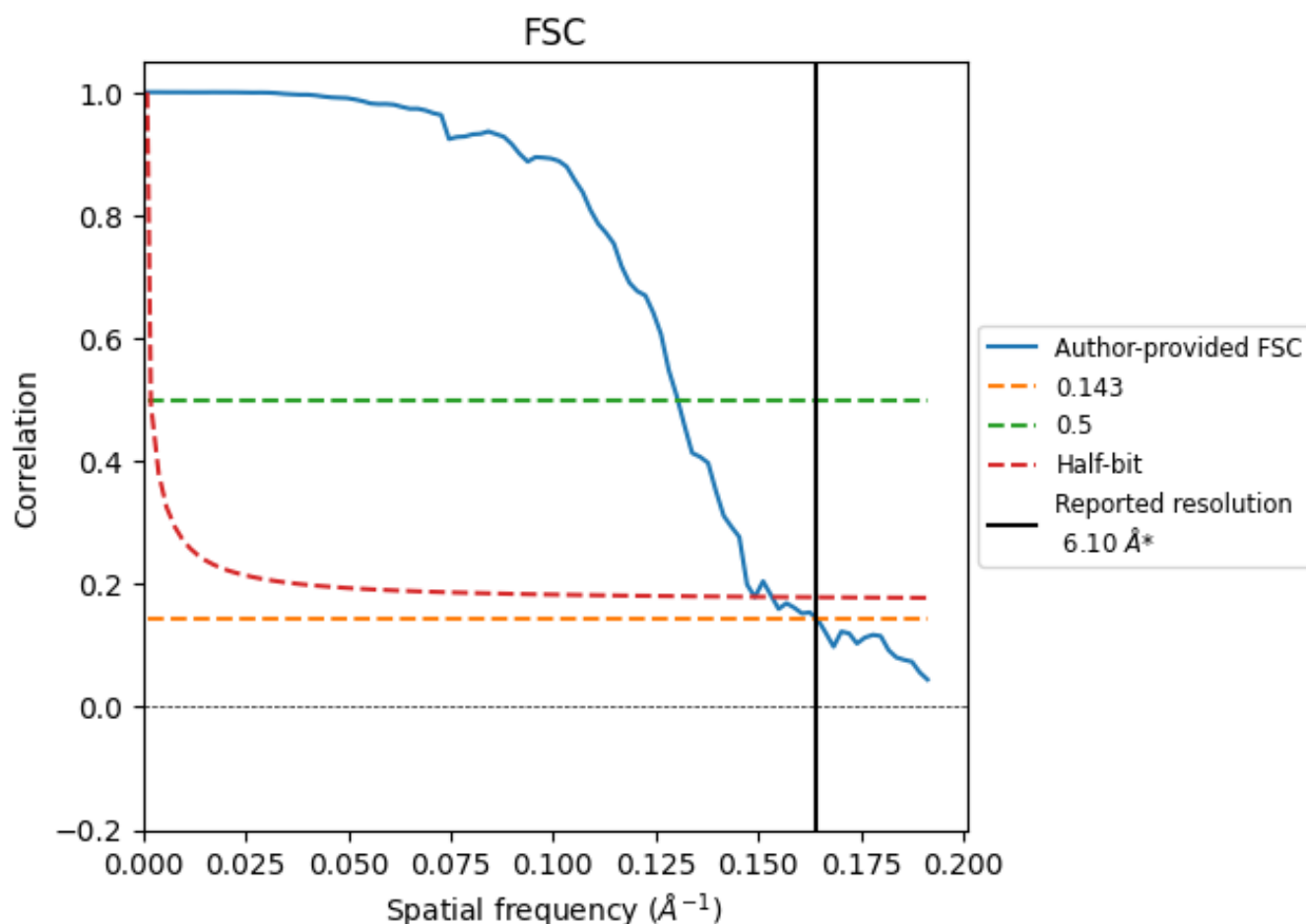


*Reported resolution corresponds to spatial frequency of 0.164 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.164 Å⁻¹

8.2 Resolution estimates [i](#)

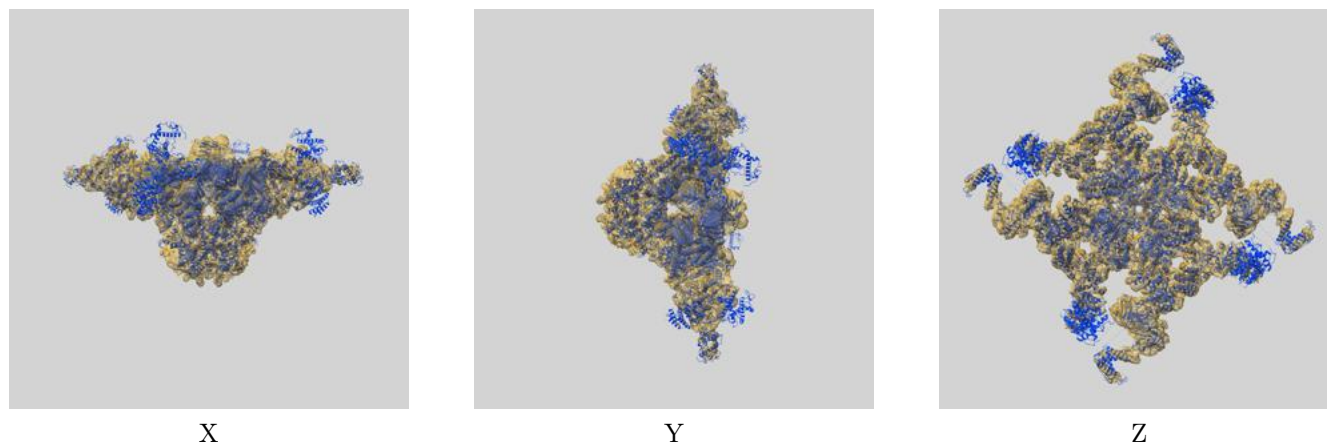
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.10	-	-
Author-provided FSC curve	6.09	7.67	6.70
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

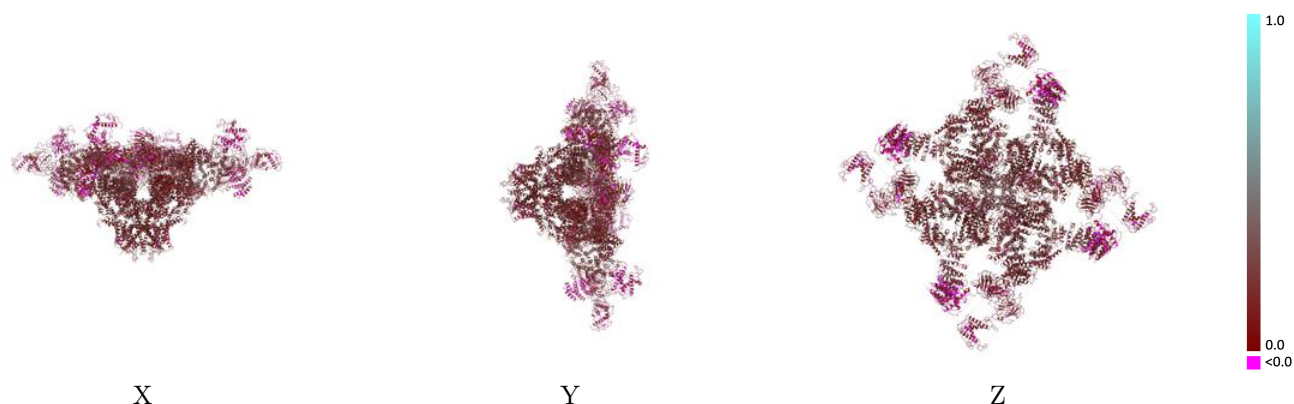
This section contains information regarding the fit between EMDB map EMD-9823 and PDB model 6JG3. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)

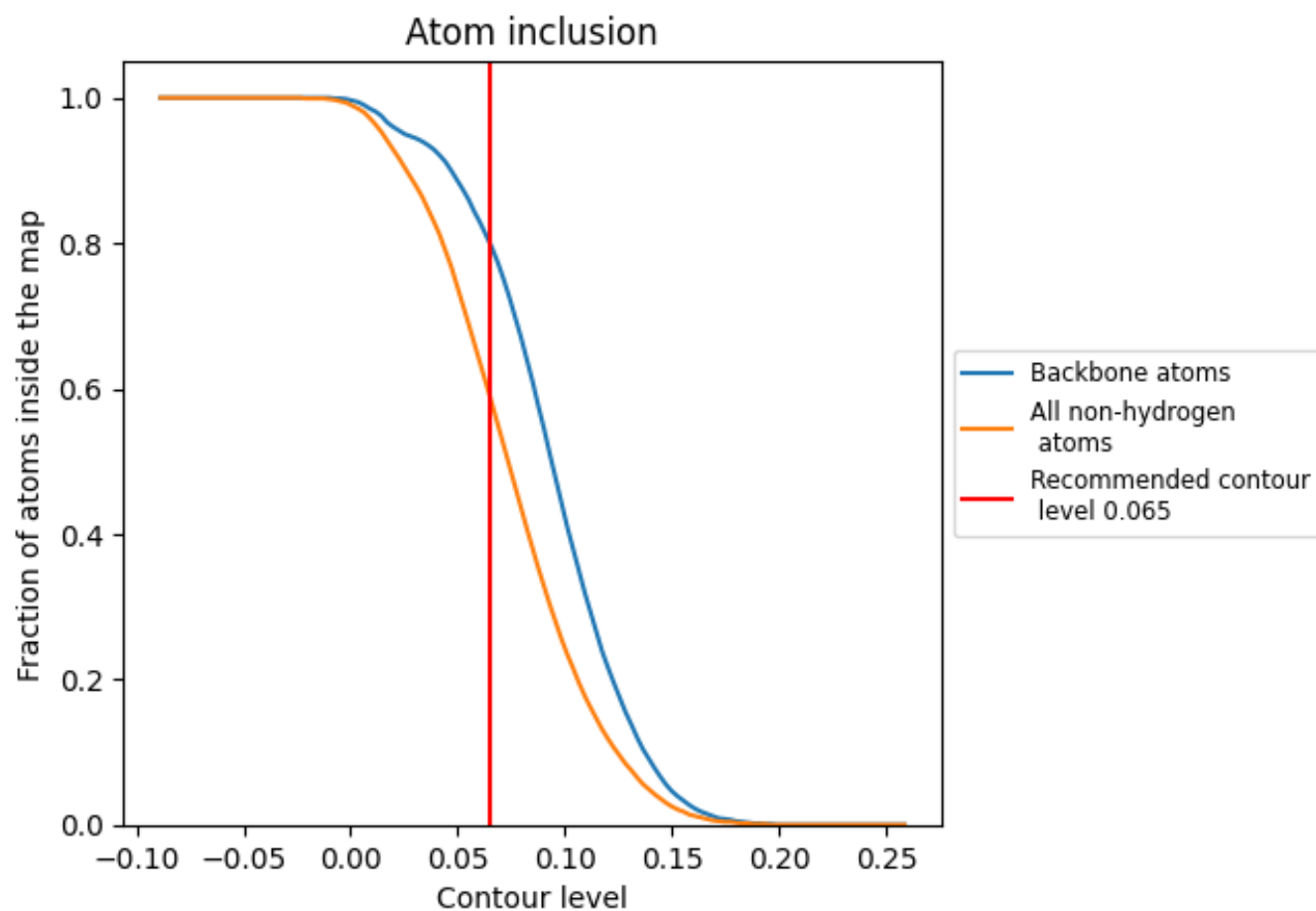


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5900	0.1840
A	0.5900	0.1830
B	0.5900	0.1850
C	0.5900	0.1840
D	0.5900	0.1840

